



IFWO

RAW SEQUENCE LISTING

DATE: 07/27/2004

PATENT APPLICATION: US/10/727,898

TIME: 13:04:45

Input Set : N:\Crf3\RULE60\10727898.raw

Output Set: N:\CRF4\07272004\J727898.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: Williams, James A.

3 Thalley, Bruce S.

4 (ii) TITLE OF INVENTION: Multivalent Vaccine For Clostridium

5 Botulinum Neurotoxin

6 (iii) NUMBER OF SEQUENCES: 82

7 (iv) CORRESPONDENCE ADDRESS:

8 (A) ADDRESSEE: Medlen & Carroll

9 (B) STREET: 220 Montgomery Street, Suite 2200

10 (C) CITY: San Francisco

11 (D) STATE: California

12 (E) COUNTRY: United States of America

13 (F) ZIP: 94104

14 (v) COMPUTER READABLE FORM:

15 (A) MEDIUM TYPE: Floppy disk

16 (B) COMPUTER: IBM PC compatible

17 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

18 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

19 (vi) CURRENT APPLICATION DATA:

C--> 20 (A) APPLICATION NUMBER: US/10/727,898

C--> 21 (B) FILING DATE: 04-Dec-2003

22 (C) CLASSIFICATION: 424

23 (vii) PRIOR APPLICATION DATA:

24 (A) APPLICATION NUMBER: US/08/704,159

25 (B) FILING DATE:

26 (viii) ATTORNEY/AGENT INFORMATION:

27 (A) NAME: Ingolia, Diane E.

28 (B) REGISTRATION NUMBER: 40,027

29 (C) REFERENCE/DOCKET NUMBER: OPHD-02304

30 (ix) TELECOMMUNICATION INFORMATION:

31 (A) TELEPHONE: (415) 705-8410

32 (B) TELEFAX: (415) 397-8338

33 (2) INFORMATION FOR SEQ ID NO: 1:

34 (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 24 base pairs

36 (B) TYPE: nucleic acid

37 (C) STRANDEDNESS: single

38 (D) TOPOLOGY: linear

39 (ii) MOLECULE TYPE: DNA (genomic)

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

41 GGAAATTTAG CTGCAGCATC TGAC

43 (2) INFORMATION FOR SEQ ID NO: 2:



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44      (i) SEQUENCE CHARACTERISTICS:
45          (A) LENGTH: 24 base pairs
46          (B) TYPE: nucleic acid
47          (C) STRANDEDNESS: single
48          (D) TOPOLOGY: linear
49      (ii) MOLECULE TYPE: DNA (genomic)
50      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
51 TCTAGCAAAT TCGCTTGTGT TGAA                                     24
53 (2) INFORMATION FOR SEQ ID NO: 3:
54      (i) SEQUENCE CHARACTERISTICS:
55          (A) LENGTH: 20 base pairs
56          (B) TYPE: nucleic acid
57          (C) STRANDEDNESS: single
58          (D) TOPOLOGY: linear
59      (ii) MOLECULE TYPE: DNA (genomic)
60      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
61 CTCGCATATA GCATTAGACC                                         20
63 (2) INFORMATION FOR SEQ ID NO: 4:
64      (i) SEQUENCE CHARACTERISTICS:
65          (A) LENGTH: 19 base pairs
66          (B) TYPE: nucleic acid
67          (C) STRANDEDNESS: single
68          (D) TOPOLOGY: linear
69      (ii) MOLECULE TYPE: DNA (genomic)
70      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
71 CTATCTAGGC CTAAAGTAT                                         19
73 (2) INFORMATION FOR SEQ ID NO: 5:
74      (i) SEQUENCE CHARACTERISTICS:
75          (A) LENGTH: 8133 base pairs
76          (B) TYPE: nucleic acid
77          (C) STRANDEDNESS: single
78          (D) TOPOLOGY: linear
79      (ii) MOLECULE TYPE: DNA (genomic)
80      (ix) FEATURE:
81          (A) NAME/KEY: CDS
82          (B) LOCATION: 1..8130
83      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
84 ATG TCT TTA ATA TCT AAA GAA GAG TTA ATA AAA CTC GCA TAT AGC ATT     48
85 Met Ser Leu Ile Ser Lys Glu Glu Leu Ile Lys Leu Ala Tyr Ser Ile
86 1      5      10      15
87 AGA CCA AGA GAA AAT GAG TAT AAA ACT ATA CTA ACT AAT TTA GAC GAA     96
88 Arg Pro Arg Glu Asn Glu Tyr Lys Thr Ile Leu Thr Asn Leu Asp Glu
89      20      25      30
90 TAT AAT AAG TTA ACT ACA AAC AAT AAT GAA AAT AAA TAT TTG CAA TTA    144
91 Tyr Asn Lys Leu Thr Thr Asn Asn Asn Glu Asn Lys Tyr Leu Gln Leu
92      35      40      45
93 AAA AAA CTA AAT GAA TCA ATT GAT GTT TTT ATG AAT AAA TAT AAA ACT    192
94 Lys Lys Leu Asn Glu Ser Ile Asp Val Phe Met Asn Lys Tyr Lys Thr
95      50      55      60

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96	TCA	AGC	AGA	AAT	AGA	GCA	CTC	TCT	AAT	CTA	AAA	AAA	GAT	ATA	TTA	AAA	240
97	Ser	Ser	Arg	Asn	Arg	Ala	Leu	Ser	Asn	Leu	Lys	Lys	Asp	Ile	Leu	Lys	
98	65				70				75						80		
99	GAA	GTA	ATT	CTT	ATT	AAA	AAT	TCC	AAT	ACA	AGC	CCT	GTA	GAA	AAA	AAT	288
100	Glu	Val	Ile	Leu	Ile	Lys	Asn	Ser	Asn	Thr	Ser	Pro	Val	Glu	Lys	Asn	
101					85				90						95		
102	TTA	CAT	TTT	GTA	TGG	ATA	GGT	GGA	GAA	GTC	AGT	GAT	ATT	GCT	CTT	GAA	336
103	Leu	His	Phe	Val	Trp	Ile	Gly	Gly	Glu	Val	Ser	Asp	Ile	Ala	Leu	Glu	
104				100				105					110				
105	TAC	ATA	AAA	CAA	TGG	GCT	GAT	ATT	AAT	GCA	GAA	TAT	AAT	ATT	AAA	CTG	384
106	Tyr	Ile	Lys	Gln	Trp	Ala	Asp	Ile	Asn	Ala	Glu	Tyr	Asn	Ile	Lys	Leu	
107			115				120						125				
108	TGG	TAT	GAT	AGT	GAA	GCA	TTC	TTA	GTA	AAT	ACA	CTA	AAA	AAG	GCT	ATA	432
109	Trp	Tyr	Asp	Ser	Glu	Ala	Phe	Leu	Val	Asn	Thr	Leu	Lys	Lys	Ala	Ile	
110			130				135						140				
111	GTT	GAA	TCT	TCT	ACC	ACT	GAA	GCA	TTA	CAG	CTA	CTA	GAG	GAA	GAG	ATT	480
112	Val	Glu	Ser	Ser	Thr	Thr	Glu	Ala	Leu	Gln	Leu	Leu	Glu	Glu	Glu	Ile	
113	145					150					155				160		
114	CAA	AAT	CCT	CAA	TTT	GAT	AAT	ATG	AAA	TTT	TAC	AAA	AAA	AGG	ATG	GAA	528
115	Gln	Asn	Pro	Gln	Phe	Asp	Asn	Met	Lys	Phe	Tyr	Lys	Lys	Arg	Met	Glu	
116				165					170						175		
117	TTT	ATA	TAT	GAT	AGA	CAA	AAA	AGG	TTT	ATA	AAT	TAT	TAT	AAA	TCT	CAA	576
118	Phe	Ile	Tyr	Asp	Arg	Gln	Lys	Arg	Phe	Ile	Asn	Tyr	Tyr	Lys	Ser	Gln	
119				180					185					190			
120	ATC	AAT	AAA	CCT	ACA	GTA	CCT	ACA	ATA	GAT	GAT	ATT	ATA	AAG	TCT	CAT	624
121	Ile	Asn	Lys	Pro	Thr	Val	Pro	Thr	Ile	Asp	Asp	Ile	Ile	Lys	Ser	His	
122			195					200						205			
123	CTA	GTA	TCT	GAA	TAT	AAT	AGA	GAT	GAA	ACT	GTA	TTA	GAA	TCA	TAT	AGA	672
124	Leu	Val	Ser	Glu	Tyr	Asn	Arg	Asp	Glu	Thr	Val	Leu	Glu	Ser	Tyr	Arg	
125			210				215							220			
126	ACA	AAT	TCT	TTG	AGA	AAA	ATA	AAT	AGT	AAT	CAT	GGG	ATA	GAT	ATC	AGG	720
127	Thr	Asn	Ser	Leu	Arg	Lys	Ile	Asn	Ser	Asn	His	Gly	Ile	Asp	Ile	Arg	
128	225					230					235				240		
129	GCT	AAT	AGT	TTG	TTT	ACA	GAA	CAA	GAG	TTA	TTA	AAT	ATT	TAT	AGT	CAG	768
130	Ala	Asn	Ser	Leu	Phe	Thr	Glu	Gln	Glu	Leu	Leu	Asn	Ile	Tyr	Ser	Gln	
131				245					250					255			
132	GAG	TTG	TTA	AAT	CGT	GGA	AAT	TTA	GCT	GCA	GCA	TCT	GAC	ATA	GTA	AGA	816
133	Glu	Leu	Leu	Asn	Arg	Gly	Asn	Leu	Ala	Ala	Ala	Ser	Asp	Ile	Val	Arg	
134				260					265					270			
135	TTA	TTA	GCC	CTA	AAA	AAT	TTT	GGC	GGA	GTA	TAT	TTA	GAT	GTT	GAT	ATG	864
136	Leu	Leu	Ala	Leu	Lys	Asn	Phe	Gly	Gly	Val	Tyr	Leu	Asp	Val	Asp	Met	
137			275					280						285			
138	CTT	CCA	GGT	ATT	CAC	TCT	GAT	TTA	TTT	AAA	ACA	ATA	TCT	AGA	CCT	AGC	912
139	Leu	Pro	Gly	Ile	His	Ser	Asp	Leu	Phe	Lys	Thr	Ile	Ser	Arg	Pro	Ser	
140			290				295							300			
141	TCT	ATT	GGA	CTA	GAC	CGT	TGG	GAA	ATG	ATA	AAA	TTA	GAG	GCT	ATT	ATG	960
142	Ser	Ile	Gly	Leu	Asp	Arg	Trp	Glu	Met	Ile	Lys	Leu	Glu	Ala	Ile	Met	
143	305					310					315				320		
144	AAG	TAT	AAA	AAA	TAT	ATA	AAT	AAT	TAT	ACA	TCA	GAA	AAC	TTT	GAT	AAA	1008

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145	Lys	Tyr	Lys	Lys	Tyr	Ile	Asn	Asn	Tyr	Thr	Ser	Glu	Asn	Phe	Asp	Lys	
146					325					330					335		
147	CTT	GAT	CAA	CAA	TTA	AAA	GAT	AAT	TTT	AAA	CTC	ATT	ATA	GAA	AGT	AAA	1056
148	Leu	Asp	Gln	Gln	Leu	Lys	Asp	Asn	Phe	Lys	Leu	Ile	Ile	Glu	Ser	Lys	
149				340					345					350			
150	AGT	GAA	AAA	TCT	GAG	ATA	TTT	TCT	AAA	TTA	GAA	AAT	TTA	AAT	GTA	TCT	1104
151	Ser	Glu	Lys	Ser	Glu	Ile	Phe	Ser	Lys	Leu	Glu	Asn	Leu	Asn	Val	Ser	
152			355					360					365				
153	GAT	CTT	GAA	ATT	AAA	ATA	GCT	TTC	GCT	TTA	GGC	AGT	GTT	ATA	AAT	CAA	1152
154	Asp	Leu	Glu	Ile	Lys	Ile	Ala	Phe	Ala	Leu	Gly	Ser	Val	Ile	Asn	Gln	
155		370					375				380						
156	GCC	TTG	ATA	TCA	AAA	CAA	GGT	TCA	TAT	CTT	ACT	AAC	CTA	GTA	ATA	GAA	1200
157	Ala	Leu	Ile	Ser	Lys	Gln	Gly	Ser	Tyr	Leu	Thr	Asn	Leu	Val	Ile	Glu	
158	385					390					395					400	
159	CAA	GTA	AAA	AAT	AGA	TAT	CAA	TTT	TTA	AAC	CAA	CAC	CTT	AAC	CCA	GCC	1248
160	Gln	Val	Lys	Asn	Arg	Tyr	Gln	Phe	Leu	Asn	Gln	His	Leu	Asn	Pro	Ala	
161				405					410					415			
162	ATA	GAG	TCT	GAT	AAT	AAC	TTC	ACA	GAT	ACT	ACT	AAA	ATT	TTT	CAT	GAT	1296
163	Ile	Glu	Ser	Asp	Asn	Asn	Phe	Thr	Asp	Thr	Thr	Lys	Ile	Phe	His	Asp	
164			420						425				430				
165	TCA	TTA	TTT	AAT	TCA	GCT	ACC	GCA	GAA	AAC	TCT	ATG	TTT	TTA	ACA	AAA	1344
166	Ser	Leu	Phe	Asn	Ser	Ala	Thr	Ala	Glu	Asn	Ser	Met	Phe	Leu	Thr	Lys	
167			435					440					445				
168	ATA	GCA	CCA	TAC	TTA	CAA	GTA	GGT	TTT	ATG	CCA	GAA	GCT	CGC	TCC	ACA	1392
169	Ile	Ala	Pro	Tyr	Leu	Gln	Val	Gly	Phe	Met	Pro	Glu	Ala	Arg	Ser	Thr	
170		450				455						460					
171	ATA	AGT	TTA	AGT	GGT	CCA	GGA	GCT	TAT	GCG	TCA	GCT	TAC	TAT	GAT	TTC	1440
172	Ile	Ser	Leu	Ser	Gly	Pro	Gly	Ala	Tyr	Ala	Ser	Ala	Tyr	Tyr	Asp	Phe	
173	465				470					475					480		
174	ATA	AAT	TTA	CAA	GAA	AAT	ACT	ATA	GAA	AAA	ACT	TTA	AAA	GCA	TCA	GAT	1488
175	Ile	Asn	Leu	Gln	Glu	Asn	Thr	Ile	Glu	Lys	Thr	Leu	Lys	Ala	Ser	Asp	
176				485					490					495			
177	TTA	ATA	GAA	TTT	AAA	TTC	CCA	GAA	AAT	AAT	CTA	TCT	CAA	TTG	ACA	GAA	1536
178	Leu	Ile	Glu	Phe	Lys	Phe	Pro	Glu	Asn	Asn	Leu	Ser	Gln	Leu	Thr	Glu	
179			500						505				510				
180	CAA	GAA	ATA	AAT	AGT	CTA	TGG	AGC	TTT	GAT	CAA	GCA	AGT	GCA	AAA	TAT	1584
181	Gln	Glu	Ile	Asn	Ser	Leu	Trp	Ser	Phe	Asp	Gln	Ala	Ser	Ala	Lys	Tyr	
182			515					520					525				
183	CAA	TTT	GAG	AAA	TAT	GTA	AGA	GAT	TAT	ACT	GGT	GGA	TCT	CTT	TCT	GAA	1632
184	Gln	Phe	Glu	Lys	Tyr	Val	Arg	Asp	Tyr	Thr	Gly	Gly	Ser	Leu	Ser	Glu	
185		530				535					540						
186	GAC	AAT	GGG	GTA	GAC	TTT	AAT	AAA	AAT	ACT	GCC	CTC	GAC	AAA	AAC	TAT	1680
187	Asp	Asn	Gly	Val	Asp	Phe	Asn	Lys	Asn	Thr	Ala	Leu	Asp	Lys	Asn	Tyr	
188	545				550					555					560		
189	TTA	TTA	AAT	AAT	AAA	ATT	CCA	TCA	AAC	AAT	GTA	GAA	GAA	GCT	GGA	AGT	1728
190	Leu	Leu	Asn	Asn	Lys	Ile	Pro	Ser	Asn	Asn	Val	Glu	Glu	Ala	Gly	Ser	
191				565					570					575			
192	AAA	AAT	TAT	GTT	CAT	TAT	ATC	ATA	CAG	TTA	CAA	GGA	GAT	GAT	ATA	AGT	1776
193	Lys	Asn	Tyr	Val	His	Tyr	Ile	Ile	Gln	Leu	Gln	Gly	Asp	Asp	Ile	Ser	

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194		580		585		590		
195	TAT	GAA	GCA	ACA	TGC	AAT	TTA	TTT
196	Tyr	Glu	Ala	Thr	Cys	Asn	Leu	Phe
197		595		600		605		
198	ATT	ATA	CAA	CGA	AAT	ATG	AAT	GAA
199	Ile	Ile	Gln	Arg	Asn	Met	Asn	Glu
200		610		615		620		
201	GAT	GAT	GGA	GAA	TCT	ATT	TTA	GAA
202	Asp	Asp	Gly	Glu	Ser	Ile	Leu	Glu
203	625			630		635		640
204	AGA	TTA	AAA	AAT	AAG	GAA	AAA	GTA
205	Arg	Leu	Lys	Asn	Lys	Glu	Lys	Val
206				645		650		655
207	AAA	GAT	GAA	TTC	AAC	ACA	AGC	GAA
208	Lys	Asp	Glu	Phe	Asn	Thr	Ser	Glu
209				660		665		670
210	CTT	TCC	AAT	GAG	ATA	AGT	TCA	TTT
211	Leu	Ser	Asn	Glu	Ile	Ser	Ser	Phe
212				675		680		685
213	TCA	CCT	AAA	AAT	GTA	GAA	GTA	AAC
214	Ser	Pro	Lys	Asn	Val	Glu	Val	Asn
215				690		695		700
216	TAT	GAT	TTT	AAT	GTT	GAA	ACT	TAT
217	Tyr	Asp	Phe	Asn	Val	Glu	Thr	Tyr
218	705			710		715		720
219	ATT	ATG	GAC	AAA	ATT	ACT	TCC	ACT
220	Ile	Met	Asp	Lys	Ile	Thr	Ser	Thr
221				725		730		735
222	ATT	ACT	ATA	GGA	GCA	AAT	CAA	TAT
223	Ile	Thr	Ile	Gly	Ala	Asn	Gln	Tyr
224				740		745		750
225	AGA	AAA	GAA	CTT	CTG	GCT	CAC	TCA
226	Arg	Lys	Glu	Leu	Leu	Ala	His	Ser
227				755		760		765
228	GCT	ATT	ATG	AGC	GAT	TTA	TCT	AGT
229	Ala	Ile	Met	Ser	Asp	Leu	Ser	Ser
230				770		775		780
231	ATA	GAT	AAT	AAG	CTA	AAA	GCA	AAG
232	Ile	Asp	Asn	Lys	Leu	Lys	Ala	Lys
233	785			790		795		800
234	TCA	ATA	TCA	GAA	GAT	ATA	AAA	ACA
235	Ser	Ile	Ser	Glu	Asp	Ile	Lys	Thr
236				805		810		815
237	CCT	GAT	ACA	AAA	TTT	ATT	TTA	AAT
238	Pro	Asp	Thr	Lys	Phe	Ile	Leu	Asn
239				820		825		830
240	TCT	ATT	GGG	GAT	TAC	ATT	TAT	TAT
241	Ser	Ile	Gly	Asp	Tyr	Ile	Tyr	Tyr
242				835		840		845

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10727898.raw

Output Set: N:\CRF4\07272004\J727898.raw

L:20 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:21 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:2911 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=32
L:7982 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=82